Long-term shedding of CTX-M-15 producing E. coli B2:ST127 by a healthy asymptomatic carrier

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Long-term shedding of CTX-M-15 producing *E. coli* B2:ST127 by a healthy asymptomatic carrier

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Sir,

Extended-spectrum ß-lactamase (ESBL) producers have become widely disseminated, particularly in Asia [1]. After a four-week stay in India, a husband and wife (53 and 52 years old, respectively) were concerned about possible exposure to resistant bacteria. Both were healthy, without histories of hospitalization or antimicrobial therapies and had not experienced gastrointestinal symptoms. Faecal swabs were taken for microbiological analysis using a commercial rectal swab tube containing Amies transport medium (Copan, Brescia, Italy). Culture of the husband's sample yielded ESBL producing Enterobacteriaceae (ESBL-ENT) and his wife tested negative. Over the next five months the husband's faecal swabs were cultured at intervals of one week, two weeks, one month, 1.5 months, 2.5 months and five months, each giving rise to ESBL-ENT. A faecal sample obtained after eight months tested negative, as did two follow-up samples taken at intervals of two and five weeks after clearance, respectively.

All isolates belonged to the virulent extraintestinal *E. coli* clone B2:ST127, harboured $bla_{\text{CTX-M-15}}$, and revealed the same PFGE pattern. One of the isolates was tested for six markers of virulence associated with uropathogenic *E. coli* (UPEC) (*traT*, *fyuA*, PAI, *chuA*, *yfcv*, *vat*) and eight marker genes of virulence associated with intestinal pathogenic *E. coli* (IPEC) (*aggR* (EAAC), *eae* (EPEC), STh, STp and LT (ETEC), *stx1* and *stx2* (STEC) and *ipaH* (EIEC)). The isolate tested positive by PCR for five of the six virulence factors that predict uropathogenicity (*fyuA*, *chuA*, PAI, *yfcv*, *vat*) but none of the virulence factors for IPEC. Mating experiments and PCR based plasmid replicon typing (PBRT) yielded negative results for all isolates, suggesting absence of a plasmid. Southern blot hybridization provided

evidence for chromosomal location of *bla*$_{\text{CTX-M-15}}$. Full genome sequencing of the first isolate (K-14KW52) revealed a chromosomally encoded *bla*$_{\text{CTX-M-15}}$ gene embedded at the right-hand extremity of an IS*Ecp1* element in a plasmid-like structure [2]. All isolates exhibited resistance to ampicillin, cephalotin, cefotaxime, streptomycin, kanamycin and sulfamethoxazole. All except one were resistant to gentamicin.

CTX-M-producing isolates have become endemic during the past decade, particularly in the community setting. This expansion is associated predominantly with the plasmid-mediated horizontal transfer of *bla*$_{\text{CTX-M}}$ genes [1] and with the spread of specific resistant clones, in particular of *E. coli* B2:ST131. Other multidrug resistant enterobacterial lineages of clinical importance include virulent extraintestinal clones belonging to phylogenetic group D such as sequence types ST38 and ST405 which are associated with *bla*$_{\text{CTX-M}}$ genes. By contrast, B2:ST127 has to date not been associated with an ESBL phenotype or with multidrug resistance [3]. However, it has recently been described as an emerging clone with an extremely high uropathogenic potential [4] and has been associated with community-acquired urinary tract infections (CAUTI) in Great Britain [3]. The detection of uropathogenic *E. coli* B2:ST127 harbouring *bla*$_{\text{CTX-M-15}}$ in a healthy person is unusual and a matter of concern, since UPEC spread easily via person-to-person contact or feco-oral transmission [5]. Notably, neither the carrier nor his wife developed symptoms of infection during the time under observation. This report is one of few that describes chromosomal location of *bla*$_{\text{CTX-M-15}}$ in *E. coli*. However, further work is necessary to assess the genetic environment of this chromosomal gene in *E. coli* B2:ST127 isolates.

Our data show that this clone can persist for at least five months in the gastrointestinal tract of a healthy individual. Prolonged carriage and shedding by asymptomatic carriers as illustrated by this case, may contribute to the dissemination of this clone.

Further studies are needed in order to assess the proportion of B2:ST127(CTX-M-15) isolates causing community acquired infections such as UTI. Increased surveillance of this clone is justified in order to limit future treatment failures.

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Ethical approval: A written agreement of the two people in view of the sampling and use of data is available.

References

[1] Cantón R, González-Alba JM, Galán JC. CTX-M enzymes: Origin and diffusion. Front Microbiol 2012;3:110.

[2] Zurfluh K, Tasara T, Stephan R. Draft genome sequence of *Escherichia coli* K-14KW52, an uropathogenic *E. coli* B2:ST127 isolate harboring a chromosomally-encoded $bla_{\text{CTX-M-15}}$ gene. Genome Announcements, accepted.

[3] Gibreel TM, Dodgson A R, Cheesbrough J, Fox AJ, Bolton FJ, Upton M. Population structure, virulence potential and antibiotic susceptibility of uropathogenic *Escherichia coli* from Northwest England. J Antimicrob Chemother 2012;67:346-56.

[4] Alghoribi MF, Gibreel TM, Dodgson AR, Beatson SA, Upton M. *Galleria mellonella* infection model demonstrates high lethality of ST69 and ST127 uropathogenic *E. coli*. PLoS One 2014;9:e101547.

[5] Foxman B. The epidemiology of urinary tract infection. Nature Rev. Urol. 2010;7:653-660.

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